



SEQUENCE LISTING

<110> Moore, Rachael
Dudley, Adam Jeston

<120> METHODS FOR THE DETECTION OF POLYMORPHISMS IN THE HUMAN OATPF GENE

<130> 06275-422US1

<150> PCT/GB03/02487
<151> 2003-06-10

<150> GB 0213580.4
<151> 2002-06-13

<150> US 60/388,692
<151> 2002-06-14

<160> 17

<170> PatentIn Ver. 2.1

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<223> Description of Artificial Sequence:PCR forward primer OATPF-1F

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<223> Description of Artificial Sequence:PCR reverse primer OATPF-1R

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<223> Description of Artificial Sequence:Validation primer

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<210> 9
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 <212> DNA
 <213> Homo sapiens

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Glu Glu Lys Gln Pro Cys Cys Gly Glu Leu Lys Val Phe Leu Cys Ala
 35 40 45

Leu Ser Phe Val Tyr Phe Ala Lys Ala Leu Ala Glu Gly Tyr Leu Lys
 50 55 60

Ser Thr Ile Thr Gln Ile Glu Arg Arg Phe Asp Ile Pro Ser Ser Leu
 65 70 75 80

Val Gly Val Ile Asp Gly Ser Phe Glu Ile Gly Asn Leu Leu Val Ile
 85 90 95

Thr Phe Val Ser Tyr Phe Gly Ala Lys Leu His Arg Pro Lys Ile Ile
 100 105 110

Gly Ala Gly Cys Val Ile Met Gly Val Gly Thr Leu Leu Ile Ala Met
 115 120 125

Pro Gln Phe Phe Met Glu Gln Tyr Lys Tyr Glu Arg Tyr Ser Pro Ser
 130 135 140

Ser Asn Ser Thr Leu Ser Ile Ser Pro Cys Leu Leu Glu Ser Ser Ser
 145 150 155 160

Gln Leu Pro Val Ser Val Met Glu Lys Ser Lys Ser Lys Ile Ser Asn
 165 170 175

Glu Cys Glu Val Asp Thr Ser Ser Ser Met Trp Ile Tyr Val Phe Leu
 180 185 190

Gly Asn Leu Leu Arg Gly Ile Gly Glu Thr Pro Ile Gln Pro Leu Gly
 195 200 205

Ile Ala Tyr Leu Asp Asp Phe Ala Ser Glu Asp Asn Ala Ala Phe Tyr
 210 215 220

Ile Gly Cys Val Gln Thr Val Ala Ile Ile Gly Pro Ile Phe Gly Phe
 225 230 235 240

Leu Leu Gly Ser Leu Cys Ala Lys Leu Tyr Val Asp Ile Gly Phe Val
 245 250 255

Asn Leu Asp His Ile Thr Ile Thr Pro Lys Asp Pro Gln Trp Val Gly
 260 265 270

Ala Trp Trp Leu Gly Tyr Leu Ile Ala Gly Ile Ile Ser Leu Leu Ala
 275 280 285

Ala Val Pro Phe Trp Tyr Leu Pro Lys Ser Leu Pro Arg Ser Gln Ser
 290 295 300

Arg Glu Asp Ser Asn Ser Ser Ser Glu Lys Ser Lys Phe Ile Ile Asp
 305 310 315 320

Asp His Thr Asp Tyr Gln Thr Pro Gln Gly Glu Asn Ala Lys Ile Met
 325 330 335

Glu Met Ala Arg Asp Phe Leu Pro Ser Leu Lys Asn Leu Phe Gly Asn
 340 345 350

Pro Val Tyr Phe Leu Tyr Leu Cys Thr Ser Thr Val Gln Phe Asn Ser
 355 360 365

Leu Phe Gly Met Val Thr Tyr Lys Pro Lys Tyr Ile Glu Gln Gln Tyr
 370 375 380

Gly Gln Ser Ser Ser Arg Ala Asn Phe Val Ile Gly Leu Ile Asn Ile
 385 390 395 400

Pro Ala Val Ala Leu Gly Ile Phe Ser Gly Gly Ile Val Met Lys Lys
 405 410 415

Phe Arg Ile Ser Val Cys Gly Ala Ala Lys Leu Tyr Leu Gly Ser Ser
 420 425 430

Val Phe Gly Tyr Leu Leu Phe Leu Ser Leu Phe Ala Leu Gly Cys Glu
 435 440 445

Asn Ser Asp Val Ala Gly Leu Thr Val Ser Tyr Gln Gly Thr Lys Pro
 450 455 460

Val Ser Tyr His Glu Arg Ala Leu Phe Ser Asp Cys Asn Ser Arg Cys
 465 470 475 480

Lys Cys Ser Glu Thr Lys Trp Glu Pro Met Cys Gly Glu Asn Gly Ile
 485 490 495

Thr Tyr Val Ser Ala Cys Leu Ala Gly Cys Gln Thr Ser Asn Arg Ser
 500 505 510

Gly Lys Asn Ile Ile Phe Tyr Asn Cys Thr Cys Val Gly Ile Ala Ala
 515 520 525

Ser Lys Ser Gly Asn Ser Ser Gly Ile Val Gly Arg Cys Gln Lys Asp
 530 535 540

Asn Gly Cys Pro Gln Met Phe Leu Tyr Phe Leu Val Ile Ser Val Ile
 545 550 555 560

Thr Ser Tyr Thr Leu Ser Leu Gly Ile Pro Gly Tyr Ile Leu Leu
 565 570 575

Leu Arg Cys Ile Lys Pro Gln Leu Lys Ser Phe Ala Leu Gly Ile Tyr
 580 585 590

Thr Leu Ala Ile Arg Val Leu Ala Gly Ile Pro Ala Pro Val Tyr Phe
 595 600 605

Gly Val Leu Ile Asp Thr Ser Cys Leu Lys Trp Gly Phe Lys Arg Cys
 610 615 620

Gly Ser Arg Gly Ser Cys Arg Leu Tyr Asp Ser Asn Val Phe Arg His
 625 630 635 640

Ile Tyr Leu Gly Leu Thr Val Ile Leu Gly Thr Val Ser Ile Leu Leu
645 650 655

Ser Ile Ala Val Leu Phe Ile Leu Lys Lys Asn Tyr Val Ser Lys His
660 665 670

Arg Ser Phe Ile Thr Lys Arg Glu Arg Thr Met Val Ser Thr Arg Phe
675 680 685

Gln Lys Glu Asn Tyr Thr Ser Asp His Leu Leu Gln Pro Asn Tyr
690 695 700

Trp Pro Gly Lys Glu Thr Gln Leu
705 710